

## SEQUENCE LISTING

<110> HEGEMANN, Peter

<120> USE OF BIOLOGICAL PHOTORECEPTORS AS DIRECTLY LIGHT-CONTROLLED  
ION CHANNELS

<130> 231181

<160> 4

<170> PatentIn version 3.1

<210> 1

<211> 712

<212> PRT

<213> Chlamydomonas reinhardtii

<220>

<223> Amino acid sequence of CHOP-1 from  
Chlamydomonas reinhardtii

<400> 1

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Met Ser Arg Arg Pro Trp Leu Leu Ala Leu Ala Leu Ala Val Ala Leu
 1           5           10           15
Ala Ala Gly Ser Ala Gly Ala Ser Thr Gly Ser Asp Ala Thr Val Pro
          20           25           30
Val Ala Thr Gln Asp Gly Pro Asp Tyr Val Phe His Arg Ala His Glu
          35           40           45
Arg Met Leu Phe Gln Thr Ser Tyr Thr Leu Glu Asn Asn Gly Ser Val
 50           55           60
Ile Cys Ile Pro Asn Asn Gly Gln Cys Phe Cys Leu Ala Trp Leu Lys
 65           70           75           80
Ser Asn Gly Thr Asn Ala Glu Lys Leu Ala Ala Asn Ile Leu Gln Trp
          85           90           95
Ile Thr Phe Ala Leu Ser Ala Leu Cys Leu Met Phe Tyr Gly Tyr Gln
          100          105          110
Thr Trp Lys Ser Thr Cys Gly Trp Glu Glu Ile Tyr Val Ala Thr Ile
          115          120          125
Glu Met Ile Lys Phe Ile Ile Glu Tyr Phe His Glu Phe Asp Glu Pro

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130	135	140										
Ala Val Ile Tyr Ser	Ser Asn Gly Asn Lys Thr Val Trp Leu Arg Tyr											
145	150	155										
Ala Glu Trp Leu	Leu Thr Cys Pro Val Ile Leu Ile His Leu Ser Asn											
	165	170										
Leu Thr Gly Leu	Ala Asn Asp Tyr Asn Lys Arg Thr Met Gly Leu Leu											
	180	185										
Val Ser Asp Ile Gly Thr Ile Val Trp Gly Thr Thr Ala Ala Leu Ser												
	195	200										
Lys Gly Tyr Val Arg Val Ile Phe Phe Leu Met Gly Leu Cys Tyr Gly												
	210	215										
Ile Tyr Thr Phe Phe Asn Ala Ala Lys Val Tyr Ile Glu Ala Tyr His												
	225	230										
Thr Val Pro Lys Gly Ile Cys Arg Asp Leu Val Arg Tyr Leu Ala Trp												
	245	250										
Leu Tyr Phe Cys Ser Trp Ala Met Phe Pro Val Leu Phe Leu Leu Gly												
	260	265										
Pro Glu Gly Phe Gly His Ile Asn Gln Phe Asn Ser Ala Ile Ala His												
	275	280										
Ala Ile Leu Asp Leu Ala Ser Lys Asn Ala Trp Ser Met Met Gly His												
	290	295										
Phe Leu Arg Val Lys Ile His Glu His Ile Leu Leu Tyr Gly Asp Ile												
	305	310										
Arg Lys Lys Gln Lys Val Asn Val Ala Gly Gln Glu Met Glu Val Glu												
	325	330										
Thr Met Val His Glu Glu Asp Asp Glu Thr Gln Lys Val Pro Thr Ala												
	340	345										
Lys Tyr Ala Asn Arg Asp Ser Phe Ile Ile Met Arg Asp Arg Leu Lys												
	355	360										
Glu Lys Gly Phe Glu Thr Arg Ala Ser Leu Asp Gly Asp Pro Asn Gly												
	370	375										
Asp Ala Glu Ala Asn Ala Ala Ala Gly Gly Lys Pro Gly Met Glu Met												
	385	390										
Gly Lys Met Thr Gly Met Gly Met Gly Met Gly Ala Gly Met Gly Met												
	405	410										
Ala Thr Ile Asp Ser Gly Arg Val Ile Leu Ala Val Pro Asp Ile Ser												
	420	425										
Met Val Asp Phe Phe Arg Glu Gln Phe Ala Arg Leu Pro Val Pro Tyr												
	435	440										
Glu Leu Val Pro Ala Leu Gly Ala Glu Asn Thr Leu Gln Leu Val Gln												
	450	455										
Gln Ala Gln Ser Leu Gly Gly Cys Asp Phe Val Leu Met His Pro Glu												

465                      470                      475                      480  
 Phe Leu Arg Asp Arg Ser Pro Thr Gly Leu Leu Pro Arg Leu Lys Met  
                                  485                      490                      495  
 Gly Gly Gln Arg Ala Ala Ala Phe Gly Trp Ala Ala Ile Gly Pro Met  
                                  500                      505                      510  
 Arg Asp Leu Ile Glu Gly Ser Gly Val Asp Gly Trp Leu Glu Gly Pro  
                                  515                      520                      525  
 Ser Phe Gly Ala Gly Ile Asn Gln Gln Ala Leu Val Ala Leu Ile Asn  
                                  530                      535                      540  
 Arg Met Gln Gln Ala Lys Lys Met Gly Met Met Gly Gly Met Gly Met  
                                  545                      550                      555                      560  
 Gly Met Gly Gly Gly Met Gly Met Gly Met Gly Met Gly Met Gly Met  
                                  565                      570                      575  
 Ala Pro Ser Met Asn Ala Gly Met Thr Gly Gly Met Gly Gly Ala Ser  
                                  580                      585                      590  
 Met Gly Gly Ala Val Met Gly Met Gly Met Gly Met Gln Pro Met Gln  
                                  595                      600                      605  
 Gln Ala Met Pro Ala Met Ser Pro Met Met Thr Gln Gln Pro Ser Met  
                                  610                      615                      620  
 Met Ser Gln Pro Ser Ala Met Ser Ala Gly Gly Ala Met Gln Ala Met  
                                  625                      630                      635                      640  
 Gly Gly Val Met Pro Ser Pro Ala Pro Gly Gly Arg Val Gly Thr Asn  
                                  645                      650                      655  
 Pro Leu Phe Gly Ser Ala Pro Ser Pro Leu Ser Ser Gln Pro Gly Ile  
                                  660                      665                      670  
 Ser Pro Gly Met Ala Thr Pro Pro Ala Ala Thr Ala Ala Pro Ala Ala  
                                  675                      680                      685  
 Gly Gly Ser Glu Ala Glu Met Leu Gln Gln Leu Met Ser Glu Ile Asn  
                                  690                      695                      700  
 Arg Leu Lys Asn Glu Leu Gly Glu  
                                  705                      710

&lt;210&gt; 2

&lt;211&gt; 737

&lt;212&gt; PRT

&lt;213&gt; Chlamydomonas reinhardtii

&lt;220&gt;

 <223> Amino acid sequence of CHOP-2 from  
 Chlamydomonas reinhardtii

&lt;400&gt; 2

## 231181.ST25.txt

Met Asp Tyr Gly Gly Ala Leu Ser Ala Val Gly Arg Glu Leu Leu Phe  
 1 5 10 15  
 Val Thr Asn Pro Val Val Val Asn Gly Ser Val Leu Val Pro Glu Asp  
 20 25 30  
 Gln Cys Tyr Cys Ala Gly Trp Ile Glu Ser Arg Gly Thr Asn Gly Ala  
 35 40 45  
 Gln Thr Ala Ser Asn Val Leu Gln Trp Leu Ala Ala Gly Phe Ser Ile  
 50 55 60  
 Leu Leu Leu Met Phe Tyr Ala Tyr Gln Thr Trp Lys Ser Thr Cys Gly  
 65 70 75 80  
 Trp Glu Glu Ile Tyr Val Cys Ala Ile Glu Met Val Lys Val Ile Leu  
 85 90 95  
 Glu Phe Phe Phe Glu Phe Lys Asn Pro Ser Met Leu Tyr Leu Ala Thr  
 100 105 110  
 Gly His Arg Val Gln Trp Leu Arg Tyr Ala Glu Trp Leu Leu Thr Cys  
 115 120 125  
 Pro Val Ile Leu Ile His Leu Ser Asn Leu Thr Gly Leu Ser Asn Asp  
 130 135 140  
 Tyr Ser Arg Arg Thr Met Gly Leu Leu Val Ser Asp Ile Gly Thr Ile  
 145 150 155 160  
 Val Trp Gly Ala Thr Ser Ala Met Ala Thr Gly Tyr Val Lys Val Ile  
 165 170 175  
 Phe Phe Cys Leu Gly Leu Cys Tyr Gly Ala Asn Thr Phe Phe His Ala  
 180 185 190  
 Ala Lys Ala Tyr Ile Glu Gly Tyr His Thr Val Pro Lys Gly Arg Cys  
 195 200 205  
 Arg Gln Val Val Thr Gly Met Ala Trp Leu Phe Phe Val Ser Trp Gly  
 210 215 220  
 Met Phe Pro Ile Leu Phe Ile Leu Gly Pro Glu Gly Phe Gly Val Leu  
 225 230 235 240  
 Ser Val Tyr Gly Ser Thr Val Gly His Thr Ile Ile Asp Leu Met Ser  
 245 250 255  
 Lys Asn Cys Trp Gly Leu Leu Gly His Tyr Leu Arg Val Leu Ile His  
 260 265 270  
 Glu His Ile Leu Ile His Gly Asp Ile Arg Lys Thr Thr Lys Leu Asn  
 275 280 285  
 Ile Gly Gly Thr Glu Ile Glu Val Glu Thr Leu Val Glu Asp Glu Ala  
 290 295 300  
 Glu Ala Gly Ala Val Asn Lys Gly Thr Gly Lys Tyr Ala Ser Arg Glu  
 305 310 315 320  
 Ser Phe Leu Val Met Arg Asp Lys Met Lys Glu Lys Gly Ile Asp Val  
 325 330 335

## 231181.ST25.txt

Arg Ala Ser Leu Asp Asn Ser Lys Glu Val Glu Gln Glu Gln Ala Ala  
 340 345 350  
 Arg Ala Ala Met Met Met Met Asn Gly Asn Gly Met Gly Met Gly Met  
 355 360 365  
 Gly Met Asn Gly Met Asn Gly Met Gly Gly Met Asn Gly Met Ala Gly  
 370 375 380  
 Gly Ala Lys Pro Gly Leu Glu Leu Thr Pro Gln Leu Gln Pro Gly Arg  
 385 390 395 400  
 Val Ile Leu Ala Val Pro Asp Ile Ser Met Val Asp Phe Phe Arg Glu  
 405 410 415  
 Gln Phe Ala Gln Leu Ser Val Thr Tyr Glu Leu Val Pro Ala Leu Gly  
 420 425 430  
 Ala Asp Asn Thr Leu Ala Leu Val Thr Gln Ala Gln Asn Leu Gly Gly  
 435 440 445  
 Val Asp Phe Val Leu Ile His Pro Glu Phe Leu Arg Asp Arg Ser Ser  
 450 455 460  
 Thr Ser Ile Leu Ser Arg Leu Arg Gly Ala Gly Gln Arg Val Ala Ala  
 465 470 475 480  
 Phe Gly Trp Ala Gln Leu Gly Pro Met Arg Asp Leu Ile Glu Ser Ala  
 485 490 495  
 Asn Leu Asp Gly Trp Leu Glu Gly Pro Ser Phe Gly Gln Gly Ile Leu  
 500 505 510  
 Pro Ala His Ile Val Ala Leu Val Ala Lys Met Gln Gln Met Arg Lys  
 515 520 525  
 Met Gln Gln Met Gln Gln Ile Gly Met Met Thr Gly Gly Met Asn Gly  
 530 535 540  
 Met Gly Gly Gly Met Gly Gly Gly Met Asn Gly Met Gly Gly Gly Asn  
 545 550 555 560  
 Gly Met Asn Asn Met Gly Asn Gly Met Gly Gly Gly Met Gly Asn Gly  
 565 570 575  
 Met Gly Gly Asn Gly Met Asn Gly Met Gly Gly Gly Asn Gly Met Asn  
 580 585 590  
 Asn Met Gly Gly Asn Gly Met Ala Gly Asn Gly Met Gly Gly Gly Met  
 595 600 605  
 Gly Gly Asn Gly Met Gly Gly Ser Met Asn Gly Met Ser Ser Gly Val  
 610 615 620  
 Val Ala Asn Val Thr Pro Ser Ala Ala Gly Gly Met Gly Gly Met Met  
 625 630 635 640  
 Asn Gly Gly Met Ala Ala Pro Gln Ser Pro Gly Met Asn Gly Gly Arg  
 645 650 655  
 Leu Gly Thr Asn Pro Leu Phe Asn Ala Ala Pro Ser Pro Leu Ser Ser  
 660 665 670

231181.ST25.txt

Gln Leu Gly Ala Glu Ala Gly Met Gly Ser Met Gly Gly Met Gly Gly  
675 680 685  
Met Ser Gly Met Gly Gly Met Gly Gly Met Gly Gly Met Gly Gly Ala  
690 695 700  
Gly Ala Ala Thr Thr Gln Ala Ala Gly Gly Asn Ala Glu Ala Glu Met  
705 710 715 720  
Leu Gln Asn Leu Met Asn Glu Ile Asn Arg Leu Lys Arg Glu Leu Gly  
725 730 735

Glu

<210> 3

<211> 259

<212> PRT

<213> Halobacterium salinarum

<220>

<223> Amino acid sequence of bacteriorhodopsin from  
Halobacterium salinarum

<400> 3

Met Leu Pro Thr Ala Val Glu Gly Val Ser Gln Ala Gln Ile Thr Gly  
1 5 10 15  
Arg Pro Glu Trp Ile Trp Leu Ala Leu Gly Thr Ala Leu Met Gly Leu  
20 25 30  
Gly Thr Leu Tyr Phe Leu Val Lys Gly Met Gly Val Ser Asp Pro Asp  
35 40 45  
Ala Lys Lys Phe Tyr Ala Ile Thr Thr Leu Val Pro Ala Ile Ala Phe  
50 55 60  
Thr Met Tyr Leu Ser Met Leu Leu Gly Tyr Gly Leu Thr Met Val Pro  
65 70 75 80  
Phe Gly Gly Glu Gln Asn Pro Ile Tyr Trp Ala Arg Tyr Ala Asp Trp  
85 90 95  
Leu Phe Thr Thr Pro Leu Leu Leu Leu Asp Leu Ala Leu Leu Val Asp  
100 105 110  
Ala Asp Gln Gly Thr Ile Leu Ala Leu Val Gly Ala Asp Gly Ile Met  
115 120 125  
Ile Gly Thr Gly Leu Val Gly Ala Leu Thr Lys Val Tyr Ser Tyr Arg  
130 135 140  
Phe Val Trp Trp Ala Ile Ser Thr Ala Ala Met Leu Tyr Ile Leu Tyr  
145 150 155 160  
Val Leu Phe Phe Gly Phe Thr Ser Lys Ala Glu Ser Met Arg Pro Glu

165 170 175  
 Val Ala Ser Thr Phe Lys Val Leu Arg Asn Val Thr Val Val Leu Trp  
 180 185 190  
 Ser Ala Tyr Pro Val Val Trp Leu Ile Gly Ser Glu Gly Ala Gly Ile  
 195 200 205  
 Val Pro Leu Asn Ile Glu Thr Leu Leu Phe Met Val Leu Asp Val Ser  
 210 215 220  
 Ala Lys Val Gly Phe Gly Leu Ile Leu Leu Arg Ser Arg Ala Ile Phe  
 225 230 235 240  
 Gly Glu Ala Glu Ala Pro Glu Pro Ser Ala Gly Asp Gly Ala Ala Ala  
 245 250 255  
 Thr Ser Asp

<210> 4  
 <211> 315  
 <212> PRT  
 <213> Chlamydomonas reinhardtii

<220>

<223> Amino acid sequence of the CHOP2-315/H134R mutant

<400> 4

Met Asp Tyr Gly Gly Ala Leu Ser Ala Val Gly Arg Glu Leu Leu Phe  
 1 5 10 15  
 Val Thr Asn Pro Val Val Val Asn Gly Ser Val Leu Val Pro Glu Asp  
 20 25 30  
 Gln Cys Tyr Cys Ala Gly Trp Ile Glu Ser Arg Gly Thr Asn Gly Ala  
 35 40 45  
 Gln Thr Ala Ser Asn Val Leu Gln Trp Leu Ala Ala Gly Phe Ser Ile  
 50 55 60  
 Leu Leu Leu Met Phe Tyr Ala Tyr Gln Thr Trp Lys Ser Thr Cys Gly  
 65 70 75 80  
 Trp Glu Glu Ile Tyr Val Cys Ala Ile Glu Met Val Lys Val Ile Leu  
 85 90 95  
 Glu Phe Phe Phe Glu Phe Lys Asn Pro Ser Met Leu Tyr Leu Ala Thr  
 100 105 110  
 Gly His Arg Val Gln Trp Leu Arg Tyr Ala Glu Trp Leu Leu Thr Cys

115

120

125

Pro Val Ile Leu Ile Arg Leu Ser Asn Leu Thr Gly Leu Ser Asn Asp  
 130 135 140

Tyr Ser Arg Arg Thr Met Gly Leu Leu Val Ser Asp Ile Gly Thr Ile  
 145 150 155 160

Val Trp Gly Ala Thr Ser Ala Met Ala Thr Gly Tyr Val Lys Val Ile  
 165 170 175

Phe Phe Cys Leu Gly Leu Cys Tyr Gly Ala Asn Thr Phe Phe His Ala  
 180 185 190

Ala Lys Ala Tyr Ile Glu Gly Tyr His Thr Val Pro Lys Gly Arg Cys  
 195 200 205

Arg Gln Val Val Thr Gly Met Ala Trp Leu Phe Phe Val Ser Trp Gly  
 210 215 220

Met Phe Pro Ile Leu Phe Ile Leu Gly Pro Glu Gly Phe Gly Val Leu  
 225 230 235 240

Ser Val Tyr Gly Ser Thr Val Gly His Thr Ile Ile Asp Leu Met Ser  
 245 250 255

Lys Asn Cys Trp Gly Leu Leu Gly His Tyr Leu Arg Val Leu Ile His  
 260 265 270

Glu His Ile Leu Ile His Gly Asp Ile Arg Lys Thr Thr Lys Leu Asn  
 275 280 285

Ile Gly Gly Thr Glu Ile Glu Val Glu Thr Leu Val Glu Asp Glu Ala  
 290 295 300

Glu Ala Gly Ala Val Asn Lys Gly Thr Gly Lys  
 305 310 315